Resource Summary Report

SIMLA

RRID:SCR_009385
Type: Tool

Proper Citation

SIMLA (RRID:SCR_009385)

Resource Information

URL: http://dmpi.duke.edu/simla-simulation-software-version-32

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Description: SIMulation program that generates data sets of families for use in Linkage and Association studies. It allows the user flexibility in specifying marker and disease placement, locus heterogeneity, disequilibrium between markers and between markers and disease loci. Output is in the form of a LINKAGE pedigree file and is easily utilized, either directly or with minimal reformatting, as input for various genetic analysis packages (entry from Genetic Analysis Software)

Synonyms: SIMulation of pedigree data for Linkage and Association studies

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++, unix, solaris, linux

Funding:

Resource Name: SIMLA

Resource ID: SCR_009385

Alternate IDs: nlx_154623

Old URLs: http://wwwchg.duhs.duke.edu/software/simla.html

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250411T055322+0000

Ratings and Alerts

No rating or validation information has been found for SIMLA.

No alerts have been found for SIMLA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Wang M, et al. (2017) A Pragmatic Test for Detecting Association between a Dichotomous Trait and the Genotypes of Affected Families, Controls and Independent Cases. Frontiers in genetics, 8, 49.